Patent Claims

1. A method for characterizing a nucleic acid fragment, wherein the following method steps are conducted:

   a) the nucleic acid fragment to be characterized is immobilized on a surface;

   b) an array of oligomers is prepared on a second surface, whereby the oligomers are provided with a label;

   c) the synthesized oligomers are stripped from the surface without leaving a pregiven region on the surface;

   d) the surface on which the nucleic acid to be characterized is immobilized is contacted with the surface of the oligomer array, whereby complementary oligomers of the array hybridize to the DNA to be characterized;

   e) non-complementary oligomers are removed;

   f) the complementary oligomers are detected by means of their label, whereby sequence information is determined on the basis of the site on the surface.

2. The method according to claim 1, further characterized in that the nucleic acid fragment to be characterized is an amplified product of genomic DNA.

3. The method according to claim 2, further characterized in that the genomic DNA is reacted with a solution of bisulfite, disulfite or hydrogen sulfite prior to the amplification.

4. The method according to one of the preceding claims, further characterized in that the nucleic acid fragment to be characterized is bound covalently to the surface.

5. The method according to claim 4, further characterized in that an amino function is introduced into the nucleic acid fragment to be characterized and this function binds to a glass surface derivatized by silanizing.

6. The method according to one of the preceding claims, further characterized in that the oligomers of the array bind covalently to the second surface.

7. The method according to one of the preceding claims, further characterized in that an amino function is introduced into the oligomers of the array and this binds to a glass surface derivatized by silanizing.

8. The method according to one of the preceding claims, further characterized in that the oligomer array is produced by solid-phase synthesis of the oligomers on the second surface.

9. The method according to claim 8, further characterized in that the solid-phase synthesis of the oligonucleotides on the second surface is

conducted in a closed synthesis chamber, and synthesis reagents are selectively introduced into this chamber.

10. The method according to claim 9, further characterized in that the oligomers are synthesized by the selective introduction of synthesis reagents to the respective sites at which the oligomers are synthesized.

11. The method according to one of the preceding claims, further characterized in that photolithographic methods and photolabile protective groups are used for the oligomer synthesis.

12. The method according to claim 11, further characterized in that electronically controllable and/or changeable masks are used for the photolithographic method.

13. The method according to claim 11, further characterized in that a mirror array, which can be switched on selectively for producing an exposure pattern, is used for the photolithographic method.

14. The method according to one of the preceding claims, further characterized in that the oligomers are synthesized in an array of cavities, which are also used, if needed, as chambers for the hybridization.

15. The method according to one of claims 1 to 13, further characterized in that the nucleic acid fragments to be characterized are immobilized on an array of cavities, which are also used, if needed, as chambers for the hybridization.

16. The method according to one of the preceding claims, further characterized in that chemical groups, which effect a change in mass and/or fluorescence, are used as labels for the oligomers.

17. The method according to one of the preceding claims, further characterized in that the hybridized oligomers are detected by means of mass spectrometry, preferably by means of matrix-assisted laser desorption/ionization mass spectrometry (MALDI).

18. The method according to one of the preceding claims, further characterized in that information on cytosine methylations in a genomic DNA sample is determined.

19. Kit for conducting the method according to one of the preceding claims, comprising reagents and/or reference nucleic acid fragments and/or reference DNA and/or treated surfaces and/or photolithographic masks and/or oligomers.